THE BIOGEOGRAPHY OF FERMENTATIVE YEAST POPULATIONS FROM THE VINEYARDS OF THE AZORES ARCHIPELAGO

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AIMS

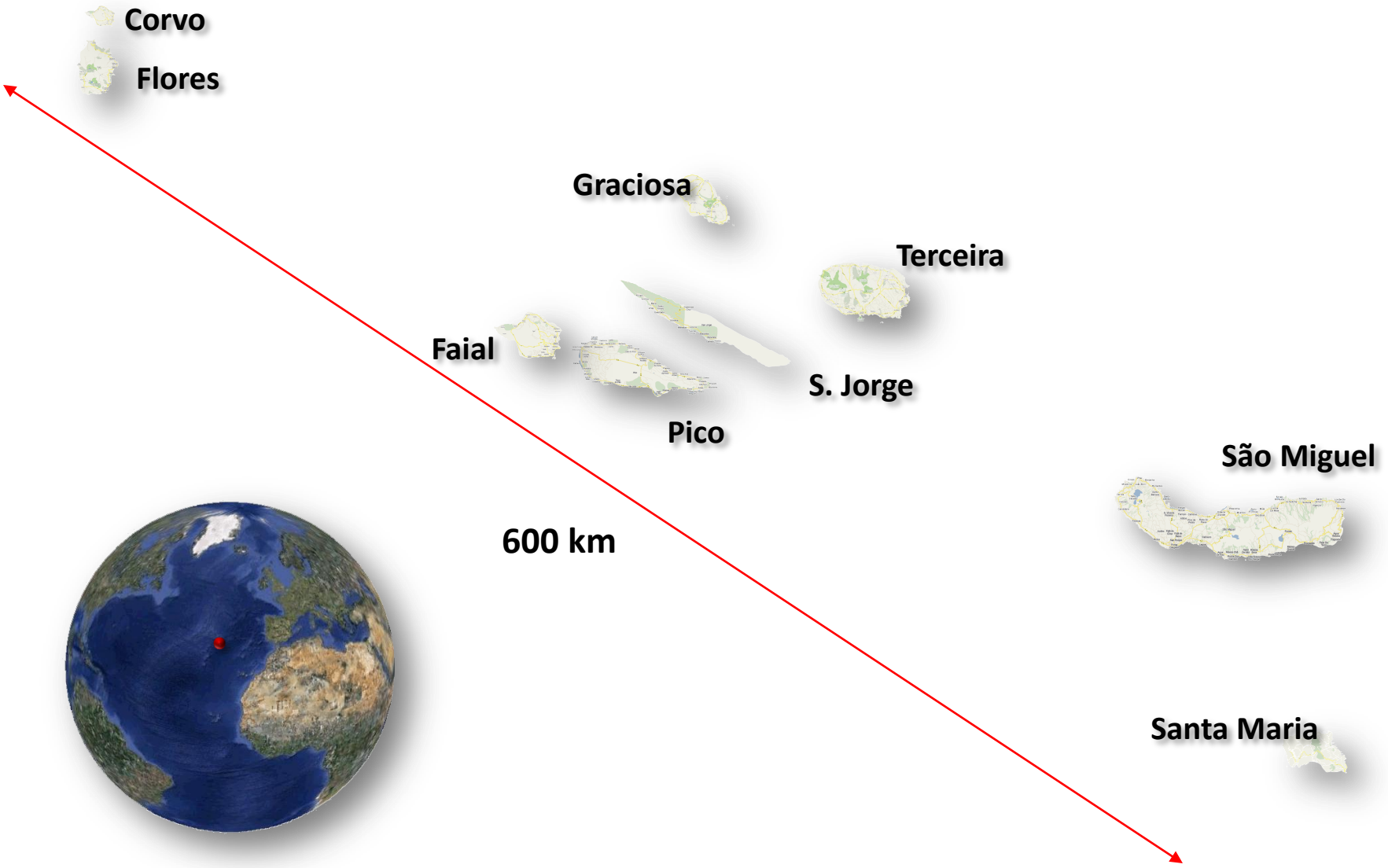
- Evaluate the biogeography of the fermentative yeast flora from the vineyards of the Azores Archipelago;

- To build a *Saccharomyces cerevisiae* strain collection as a resource for:

  - Preservation of yeast genetic diversity;
  - Selection and improvement of wine strains;
  - Equitable sharing of genetic data;
  - Evolutionary studies of this species in isolated island environments.

INTRODUCTION

Azores Archipelago

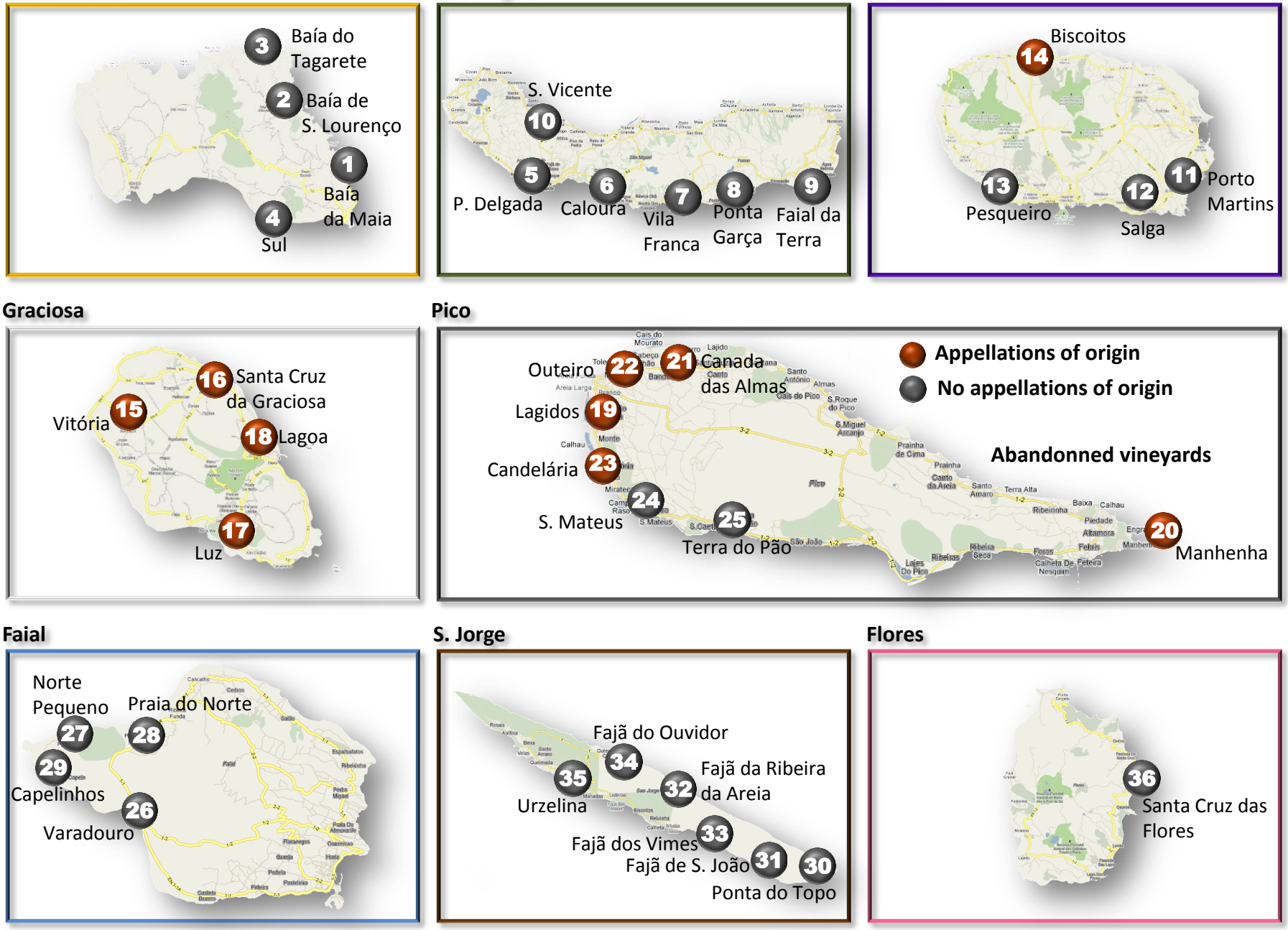


Non-abandoned vineyards

Abandoned vineyards

MATERIAL AND METHODS

SAMPLING LOCATIONS



MATERIAL AND METHODS

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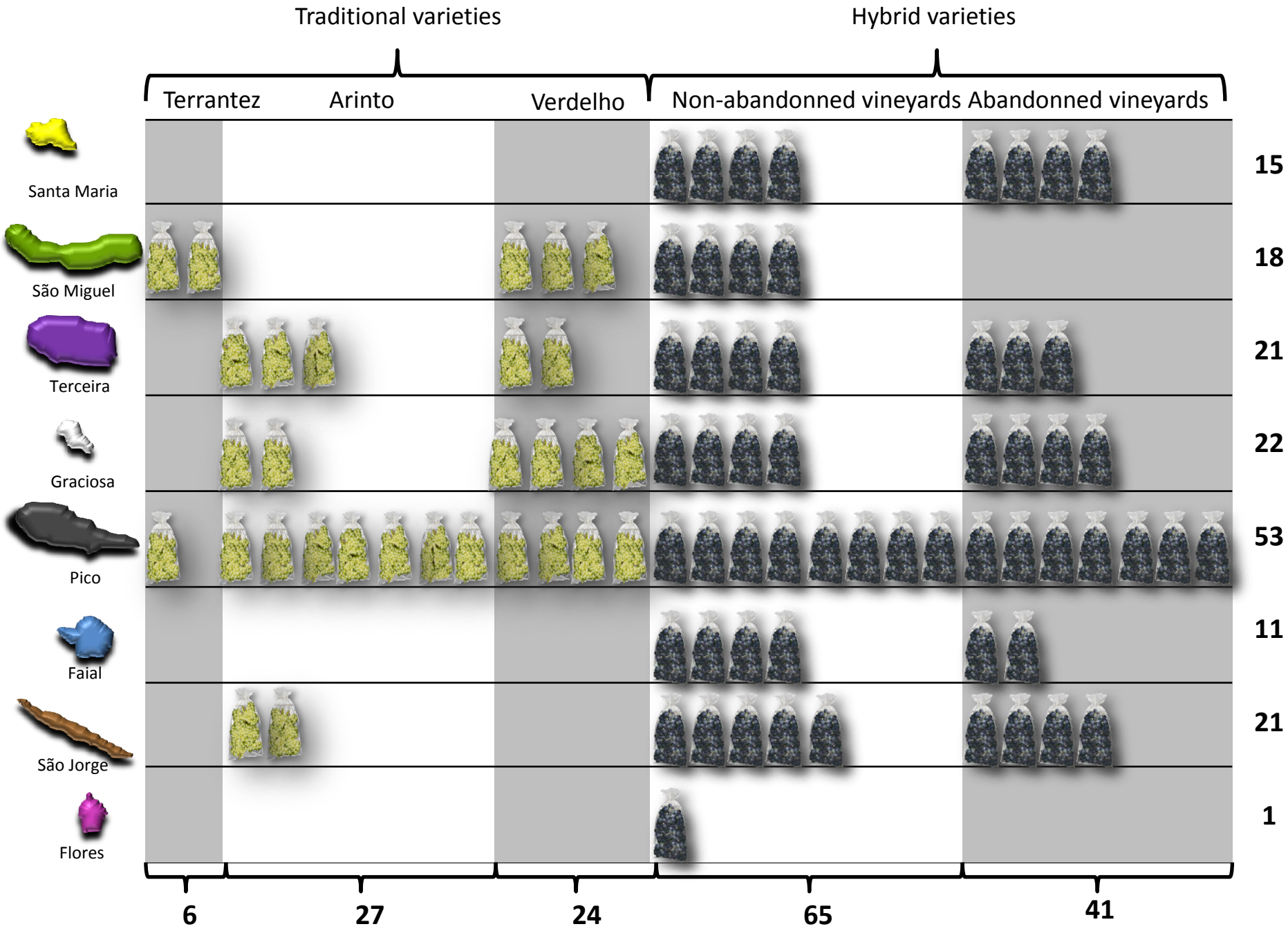
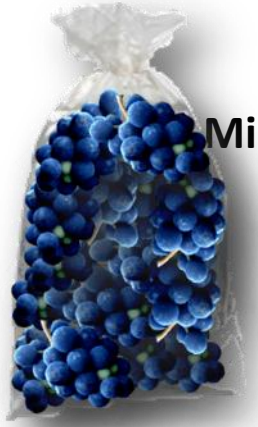
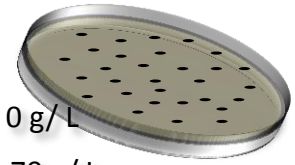


MATERIAL AND METHODS



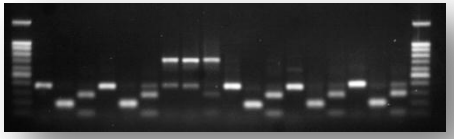
Microvinification

Isolation



Species identification

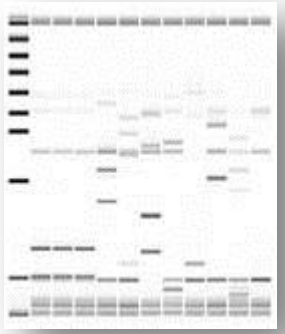
ITS-RFLP

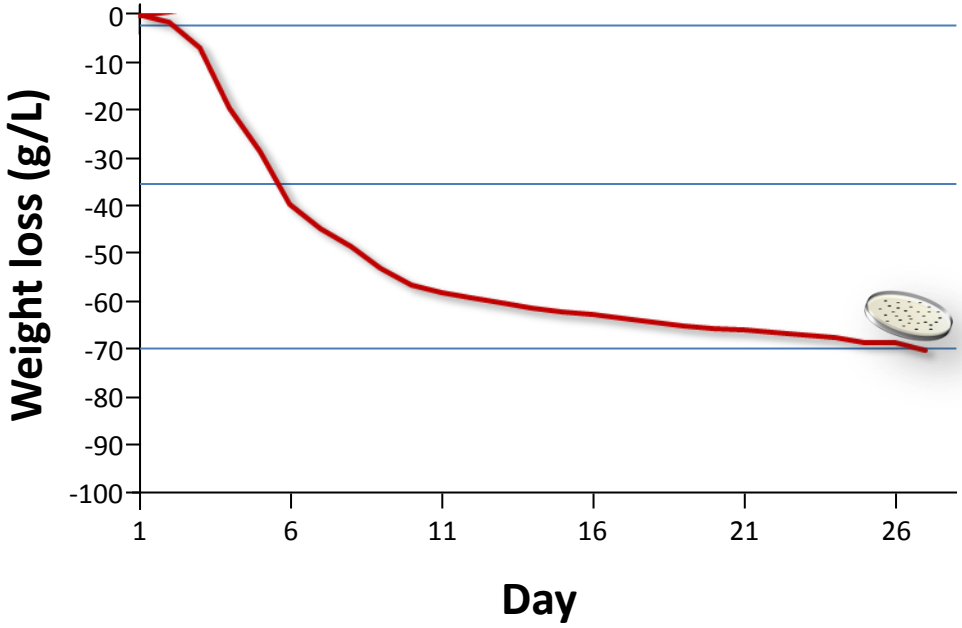


SEQUENCING

S. cerevisiae strains identification

Interdelta Sequences



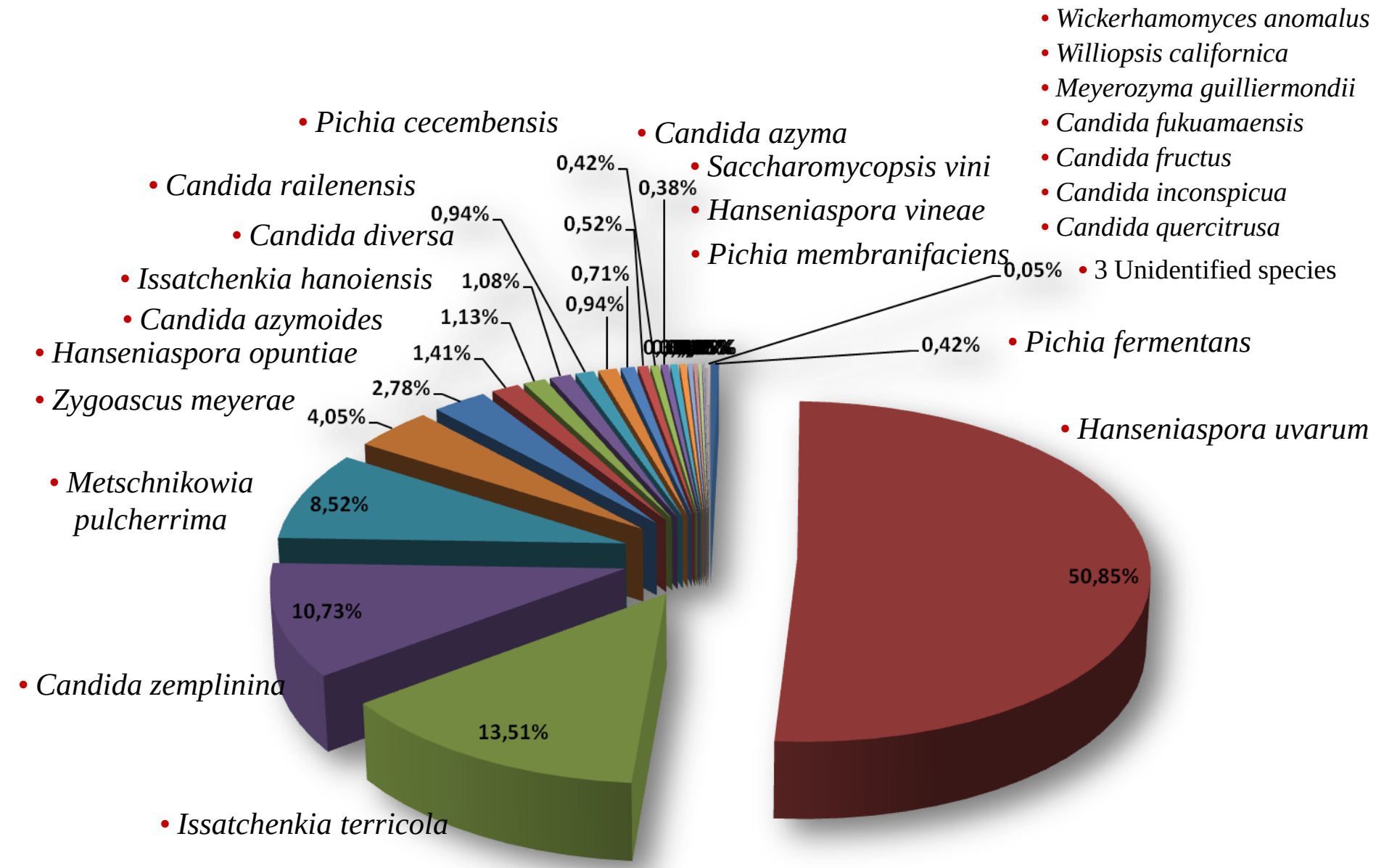


RESULTS

Number of yeast isolates

	Fermentation initial stage	Fermentation final stage	Total
2009	2640	1470	4110
2010	2250	1170	3420
Total	4890	2640	7530

RESULTS Yeast species occurring in initial fermentative stages



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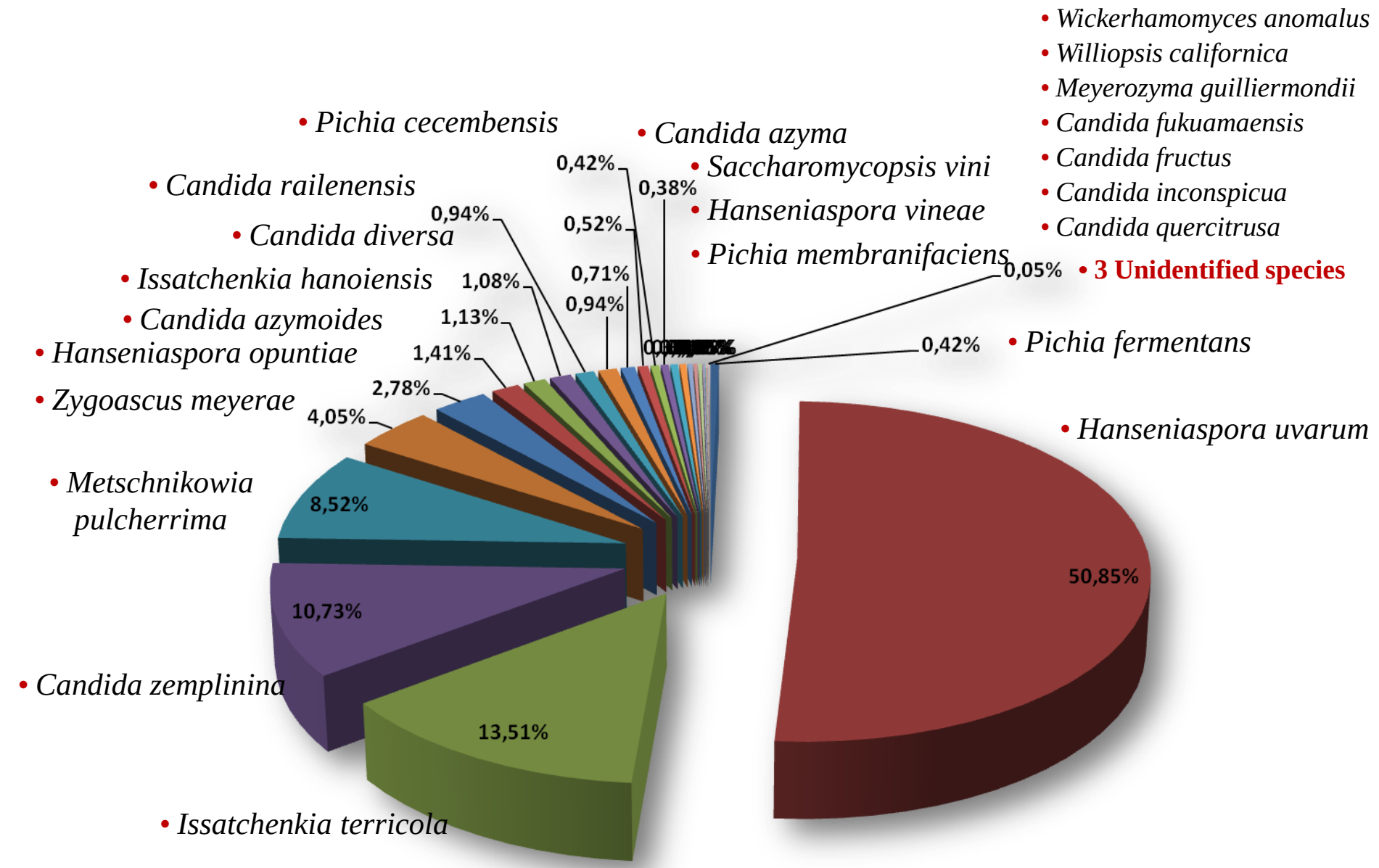

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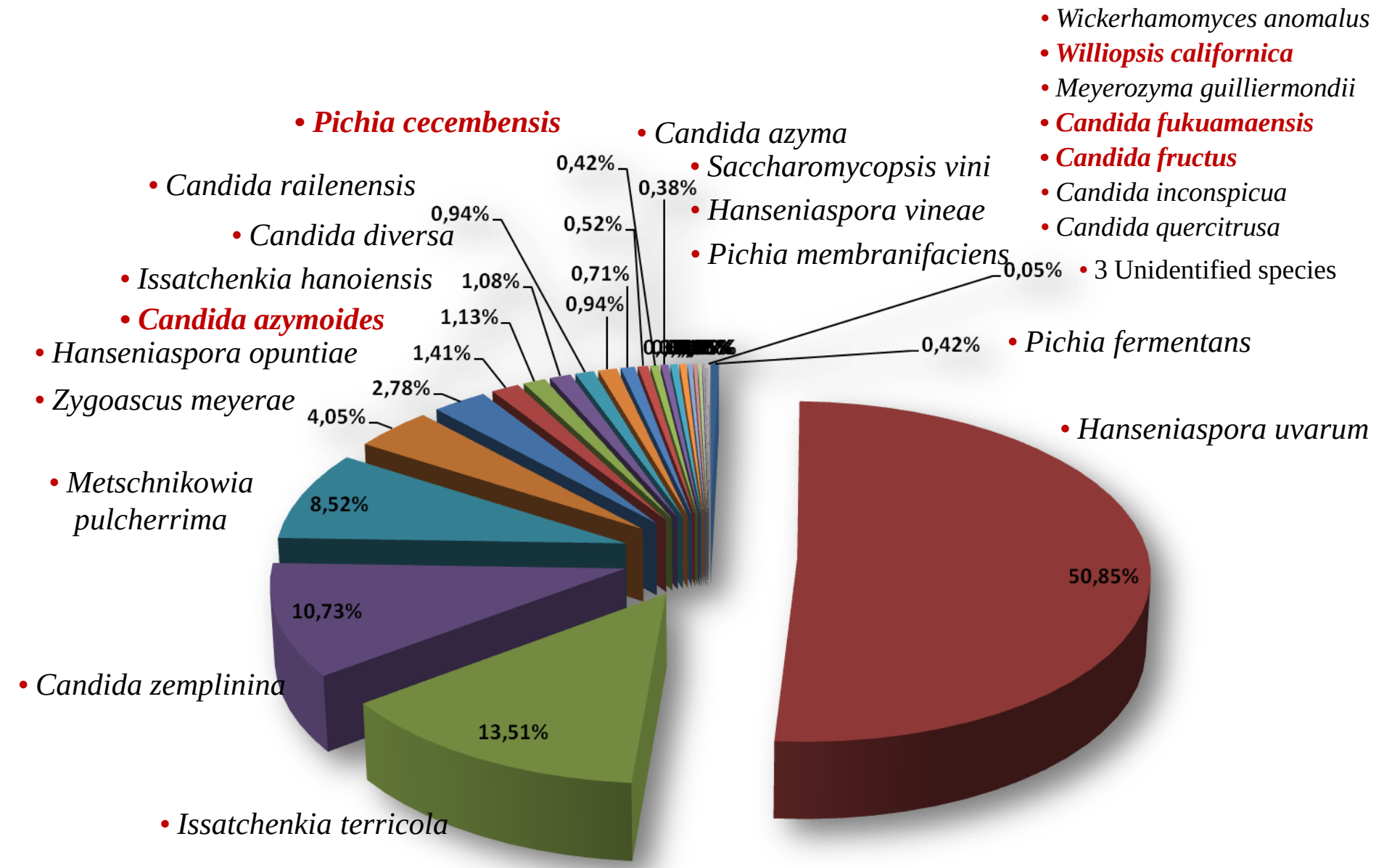

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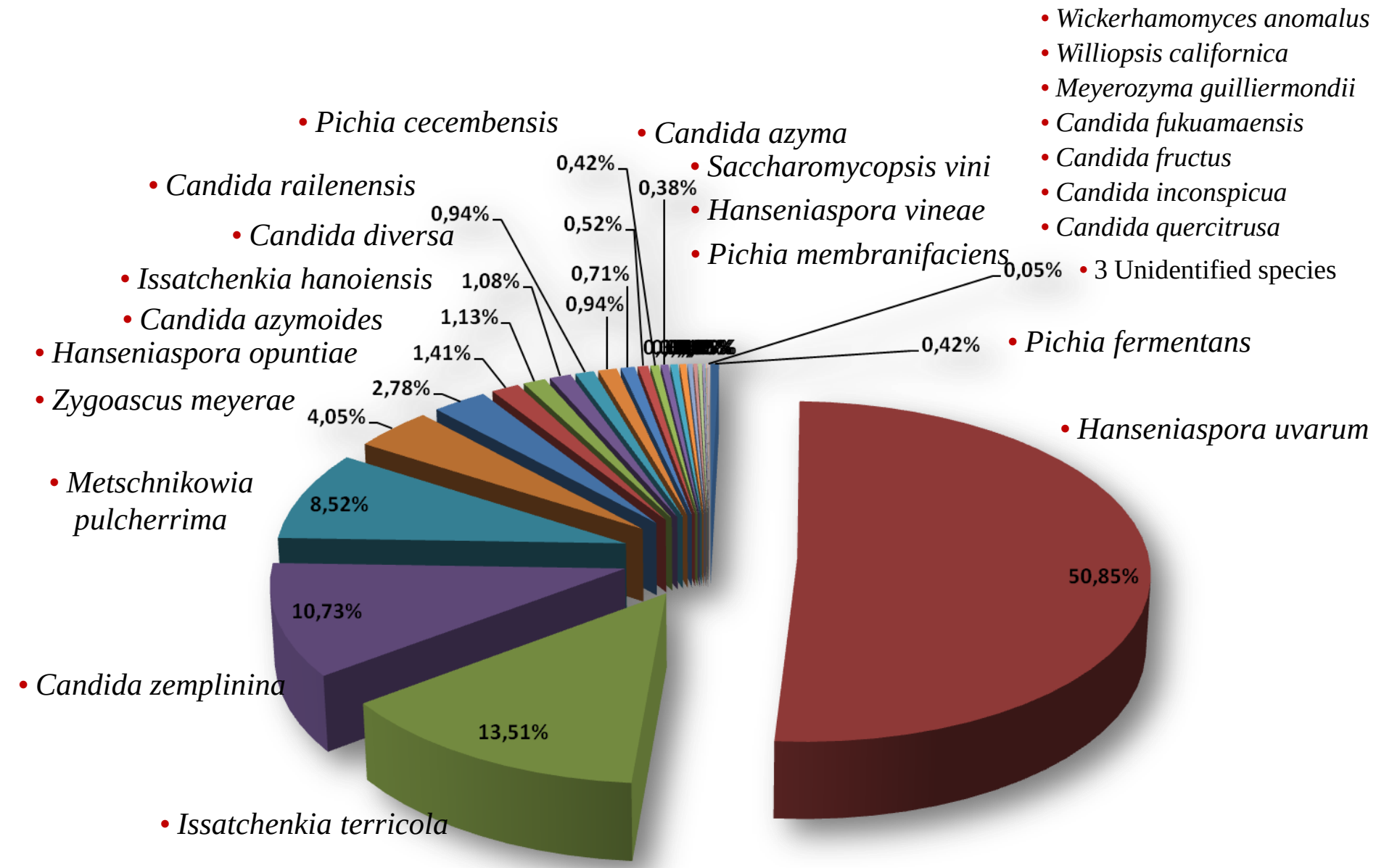

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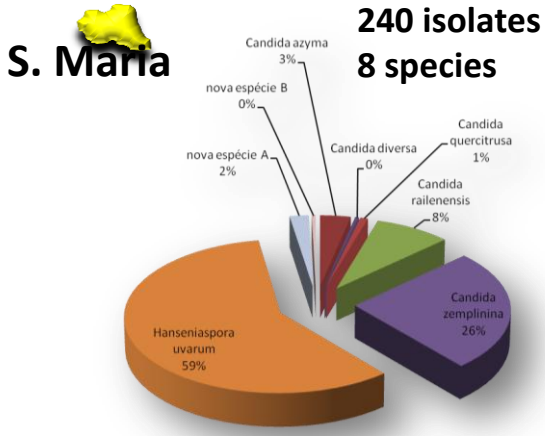

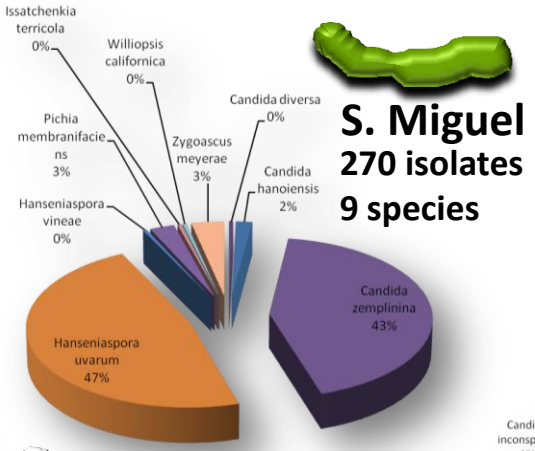

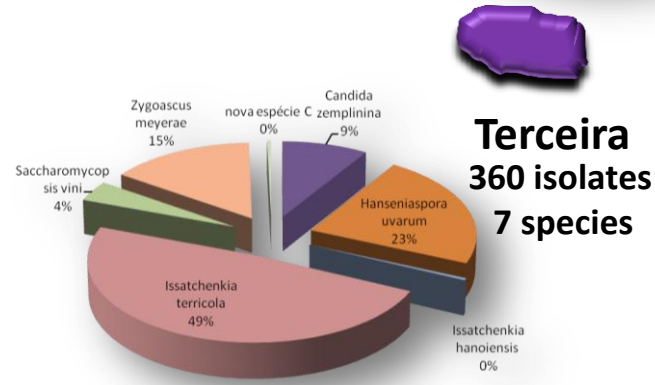

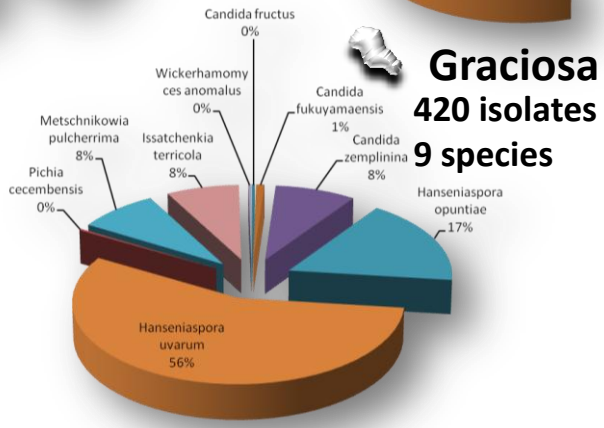

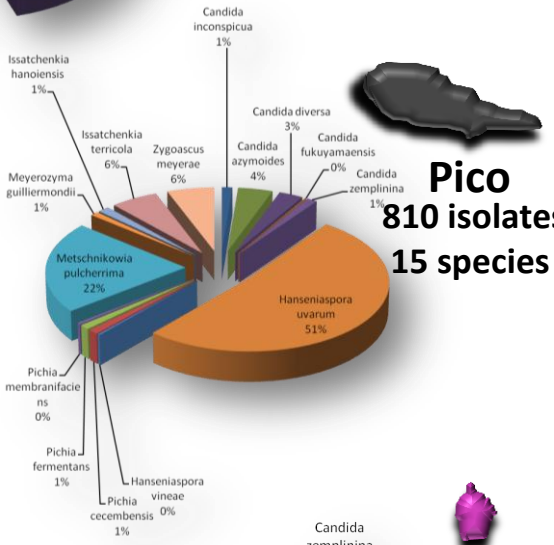

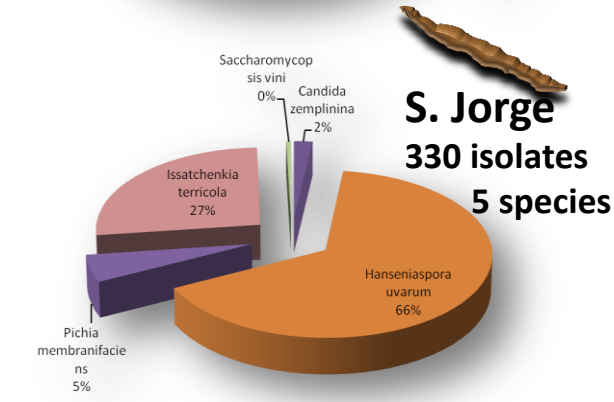

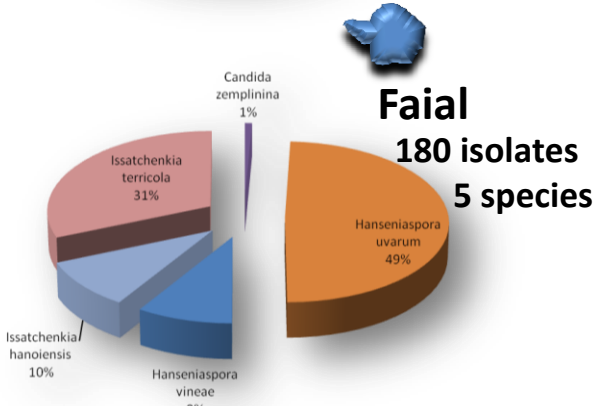

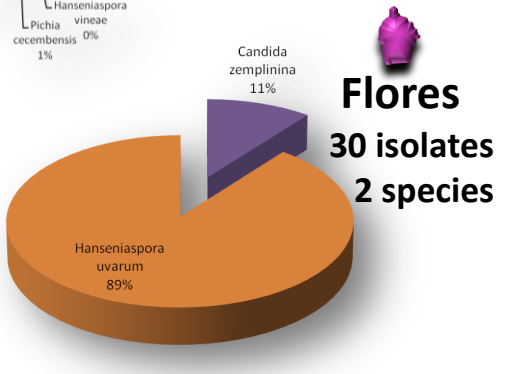

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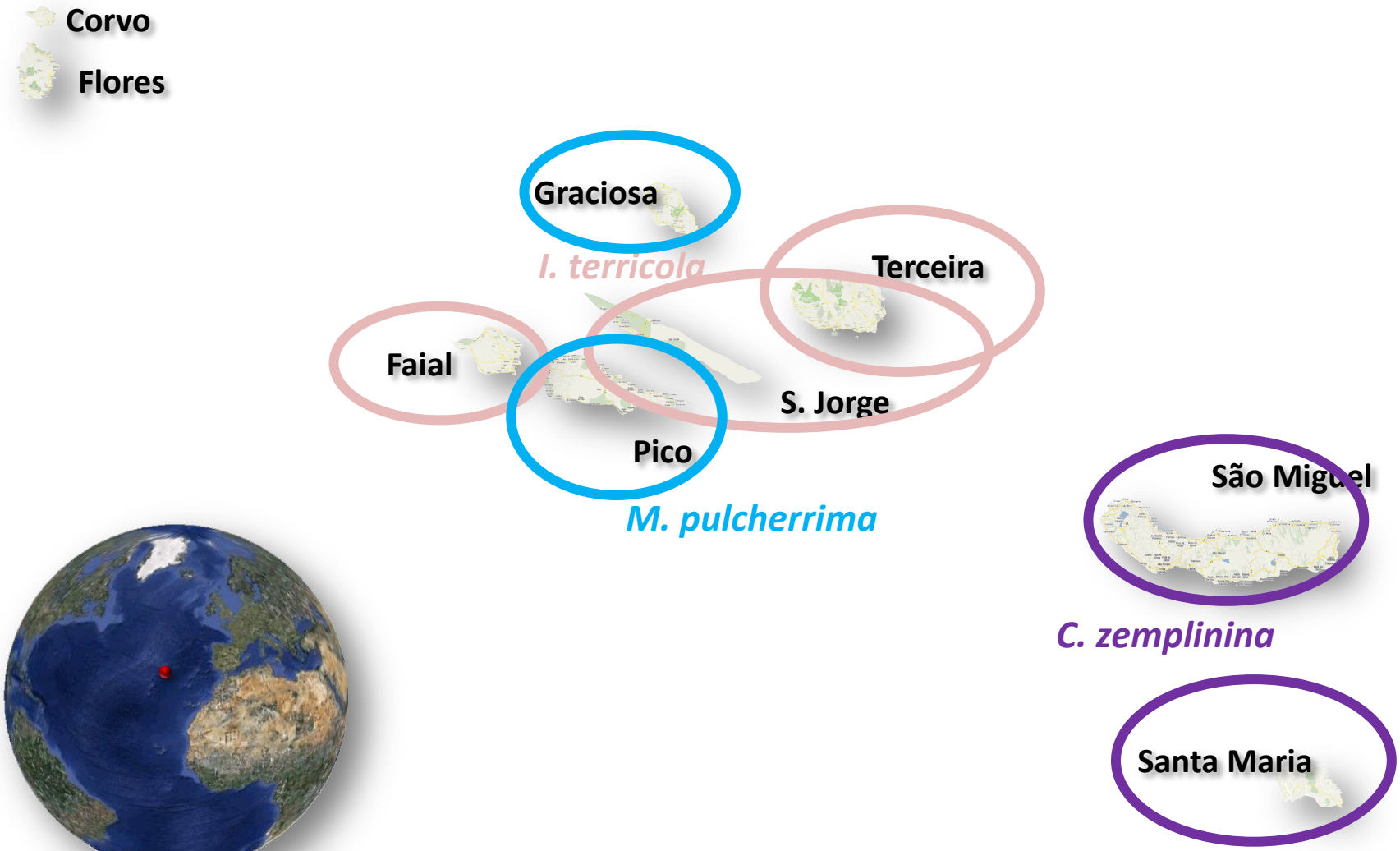

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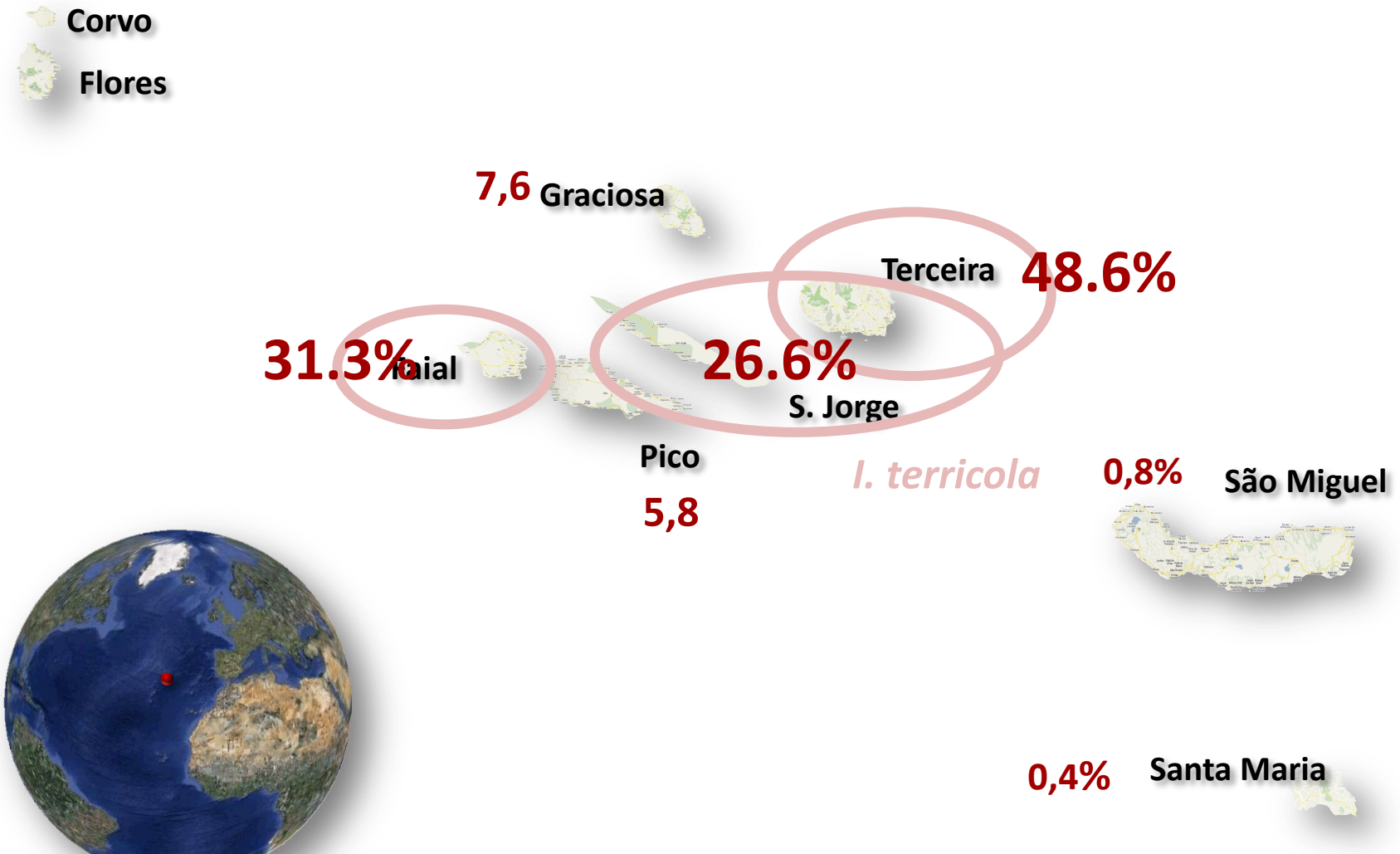

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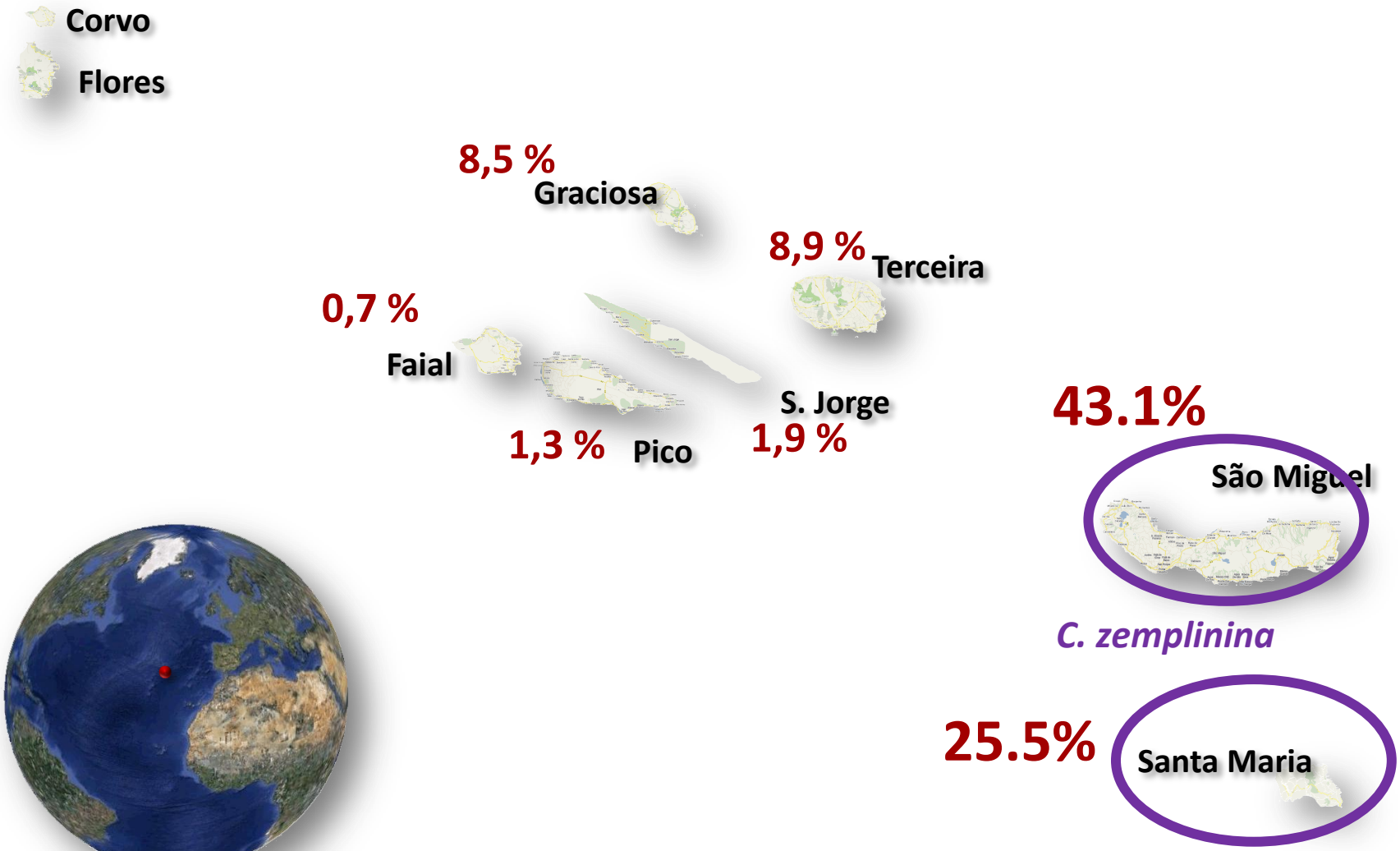

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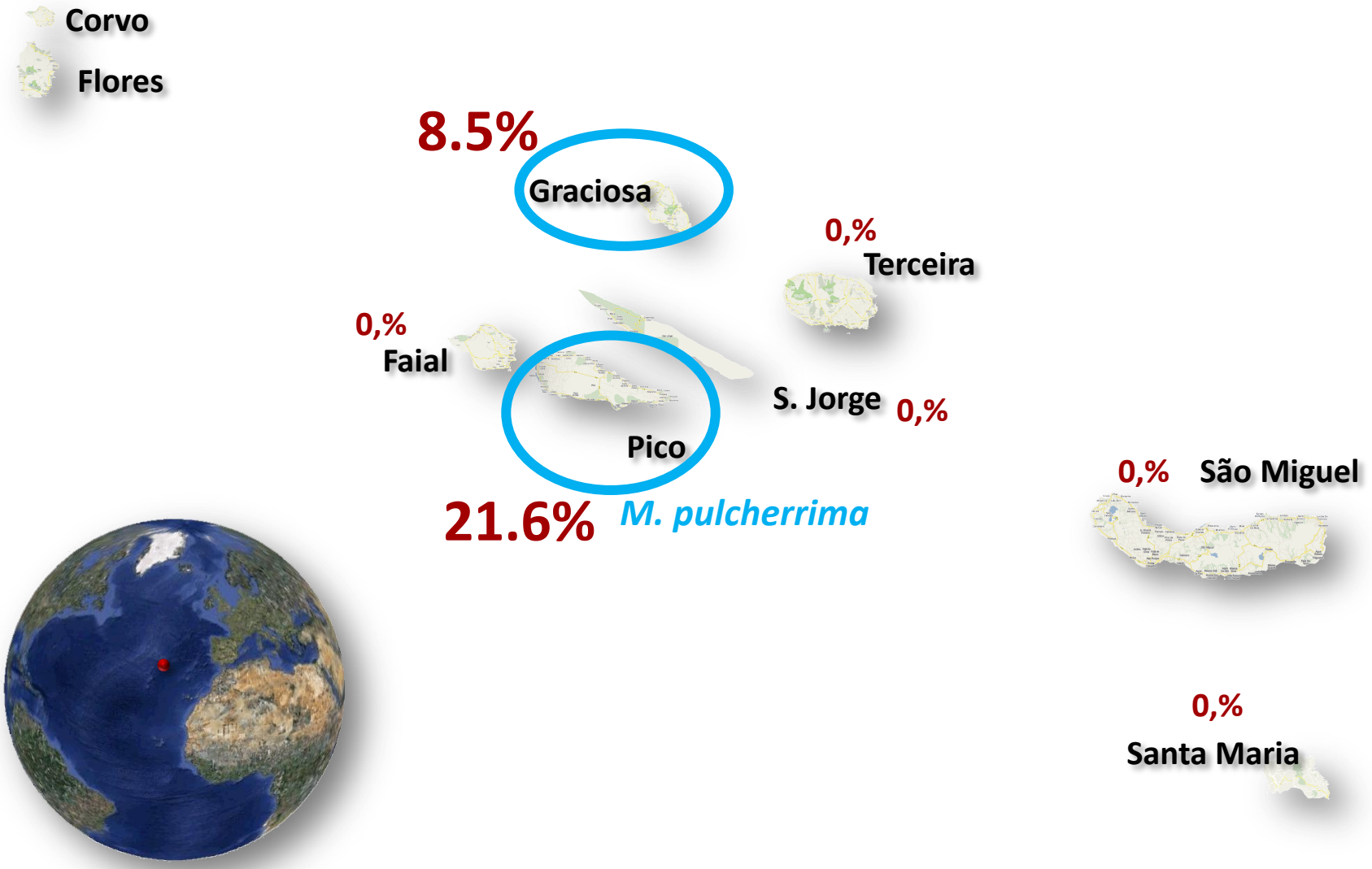
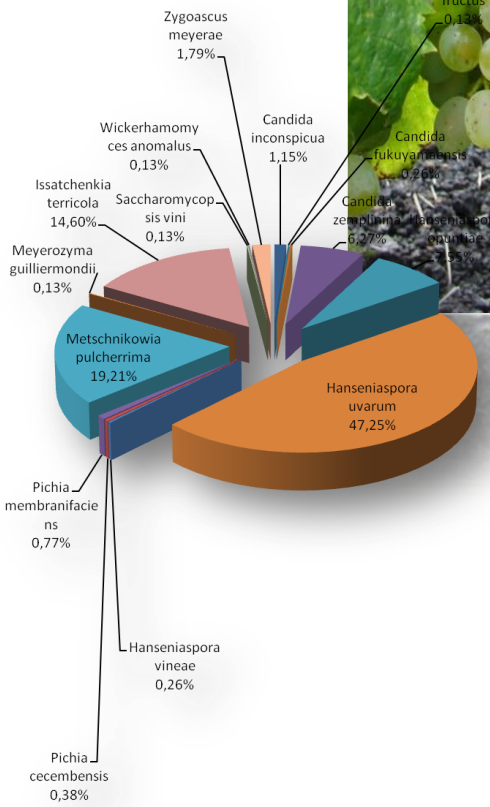
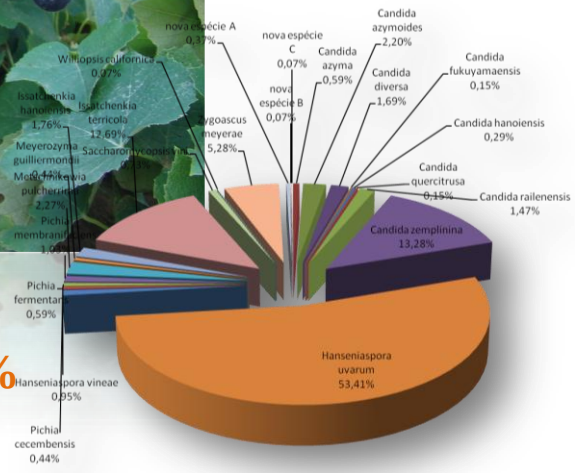


RESULTS Yeast species occurring in initial fermentative stages

Traditional varieties



Hybrid varieties



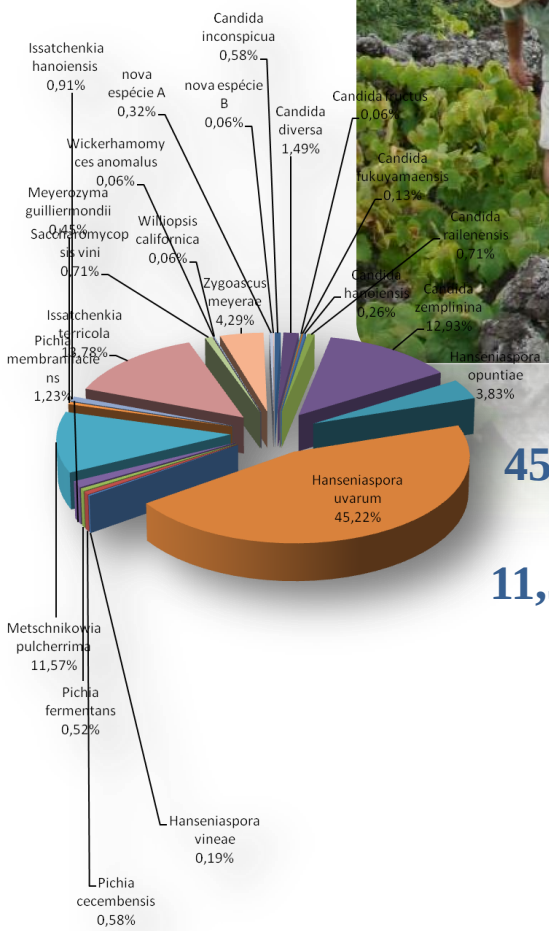
47,25 % *Hanseniaspora uvarum* 53,41 %

19,21 % *Metschnikowia pulcherrima* 2,27%

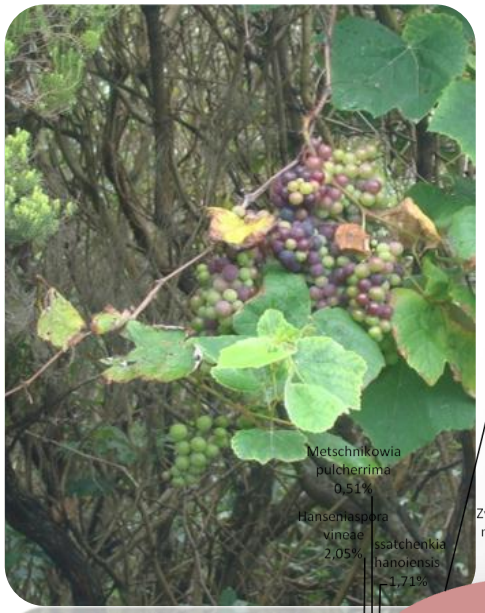
14,60% *Candida zemplinina* 12,69 %

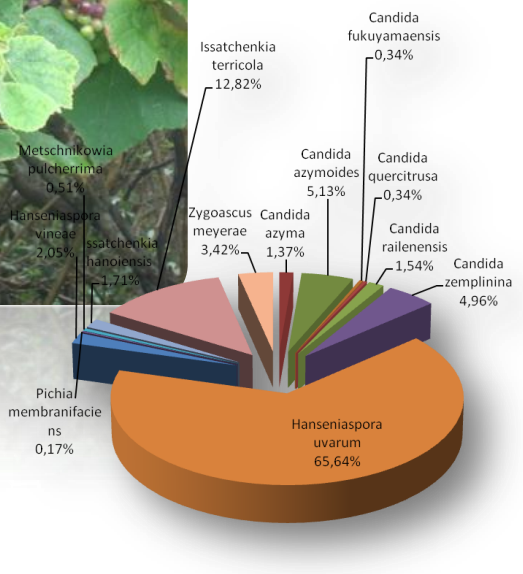
RESULTS Yeast species occurring in initial fermentative stages

Non-abandoned vineyards



Abandoned vineyards





45,22 % *Hanseniaspora uvarum* 65,64 %

11,57 % *Metschnikowia pulcherrima* 0,51%

0 % *Candida azymoides* 5,13%

RESULTS

Number of yeast isolates

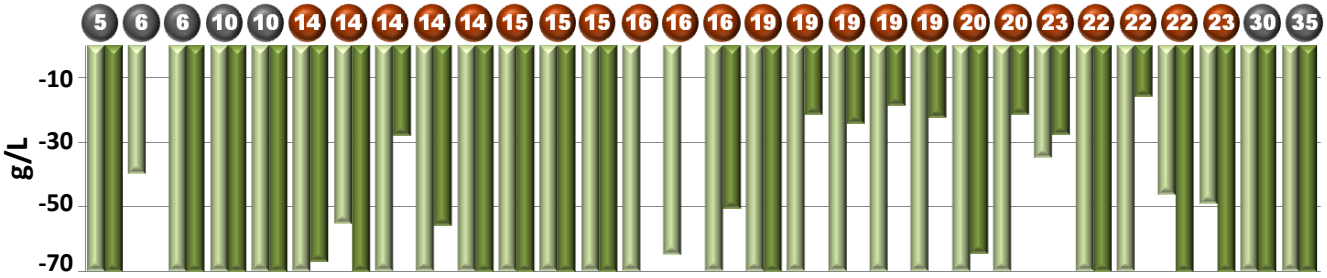
	Fermentation initial stage	Fermentation final stage	Total
2009	2640	1470	4110
2010	2250	1170	3420
Total	4890	2640	7530

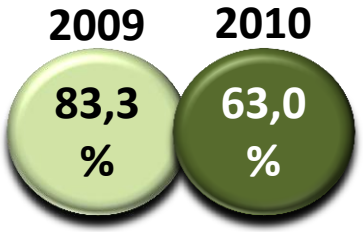
RESULTS

Fermentations data

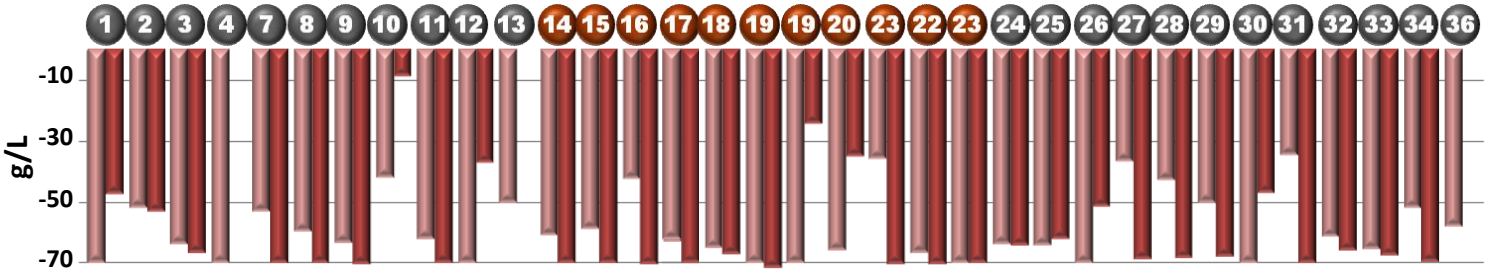
Finished fermentations

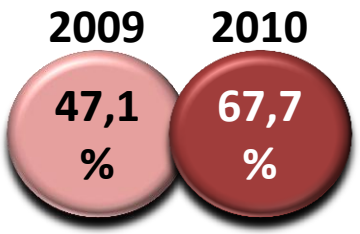
SAMPLES OF TRADITIONAL VARIETIES FROM NON-ABANDONED VINEYARDS



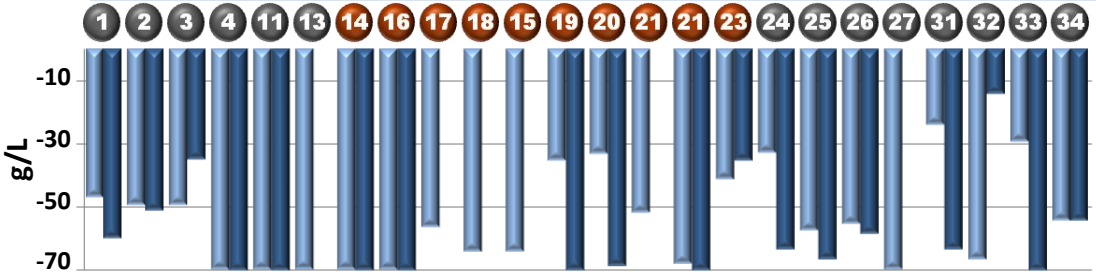


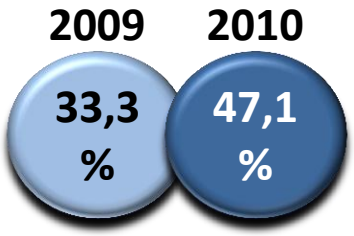
SAMPLES OF HYBRID VARIETIES FROM NON-ABANDONED VINEYARDS





SAMPLES OF HYBRID VARIETIES FROM ABANDONED VINEYARDS





Samples from appellations of origin

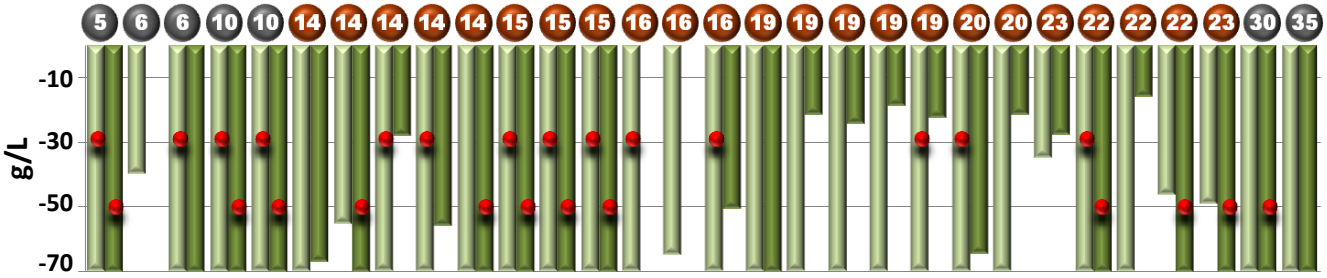
Samples from other winemaking regions

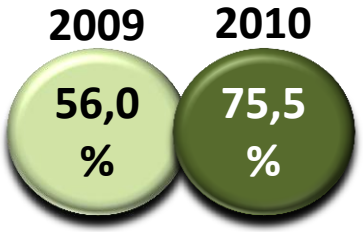
RESULTS

Fermentations data

Fermentations finished by *S. cerevisiae*

SAMPLES OF TRADITIONAL VARIETIES FROM NON-ABANDONED VINEYARDS





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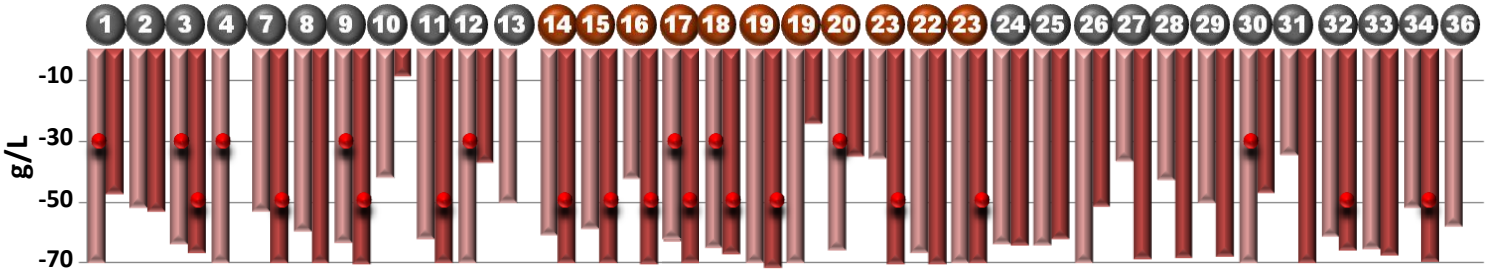
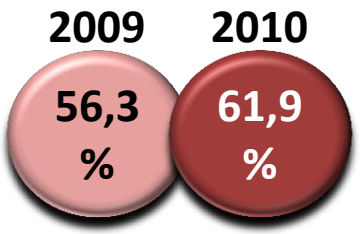
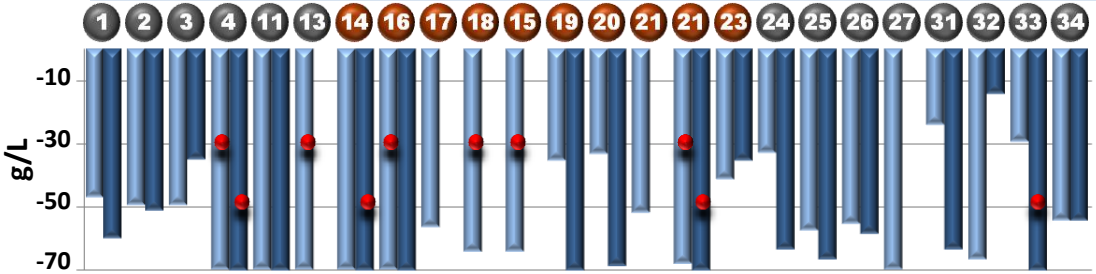
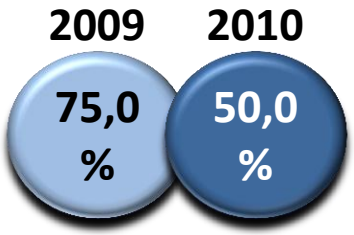




SAMPLES OF HYBRID VARIETIES FROM ABANDONED VINEYARDS





Fermentations completed by *S. cerevisiae*

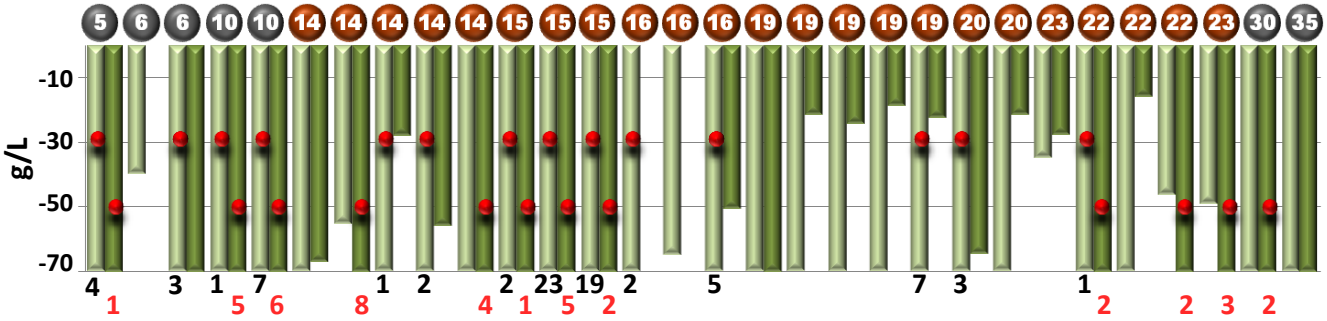
Samples from appellations of origin

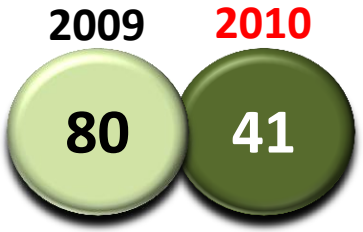
Samples from other winemaking regions

RESULTS *S. cerevisiae* microflora composition

Total number of *S. cerevisiae* strains

SAMPLES OF TRADITIONAL VARIETIES FROM NON-ABANDONED VINEYARDS





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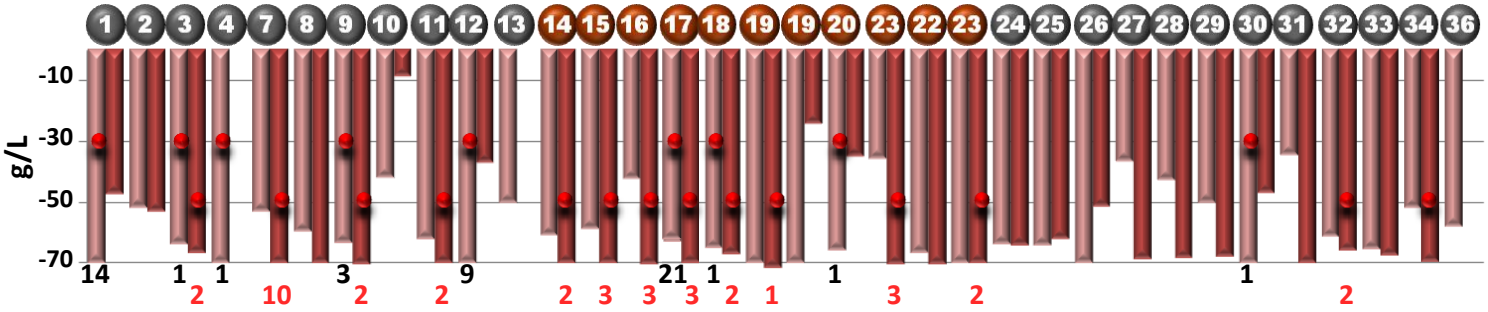
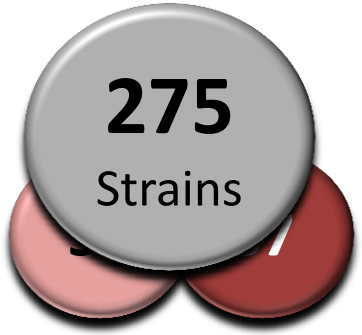
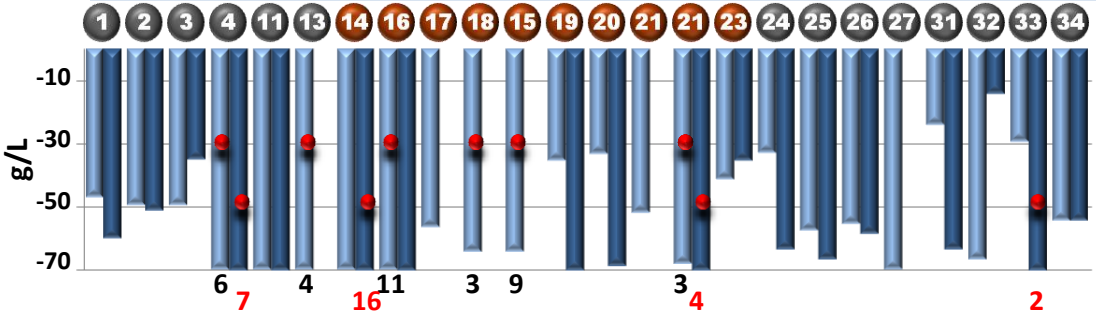
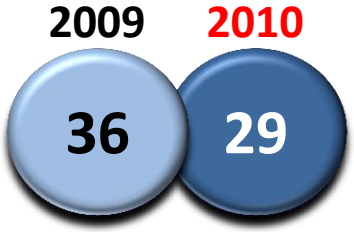




SAMPLES OF HYBRID VARIETIES FROM ABANDONED VINEYARDS





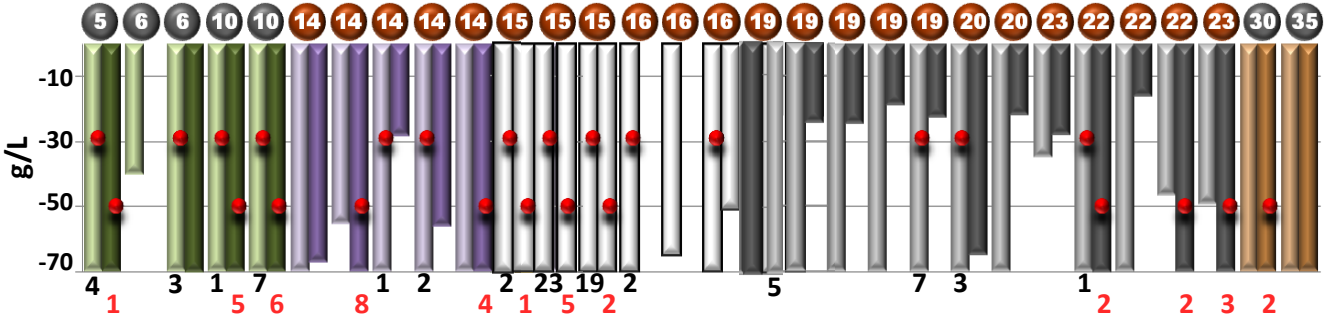
Fermentations completed by *S. cerevisiae*

Samples from appellations of origin

Samples from other winemaking regions

RESULTS *S. cerevisiae* microflora composition per island

SAMPLES OF TRADITIONAL VARIETIES FROM NON-ABANDONED VINEYARDS



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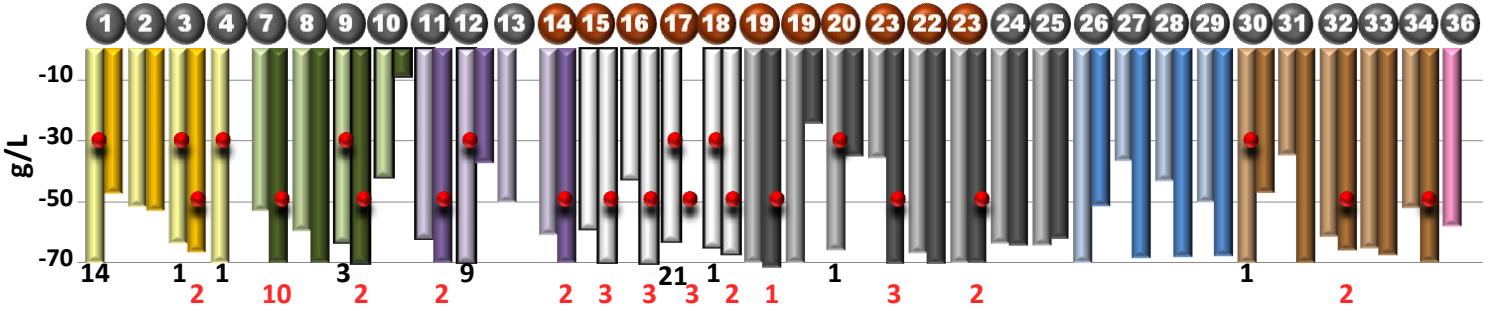

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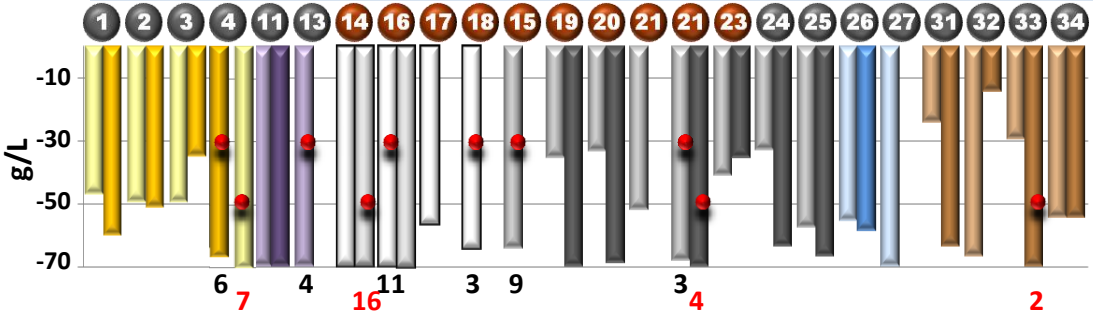

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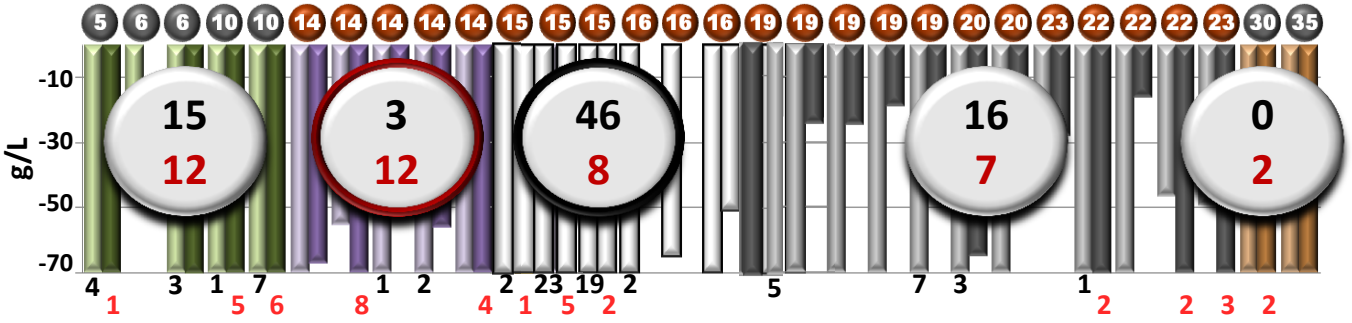
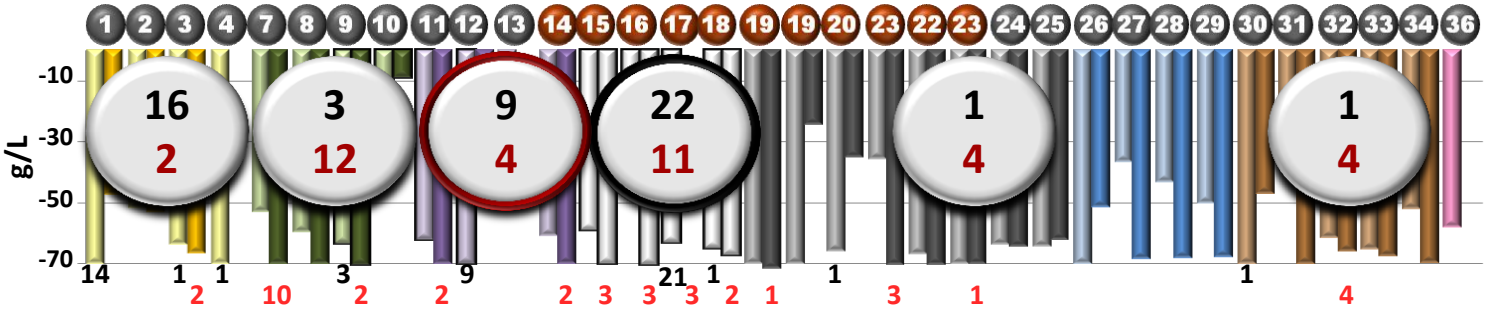
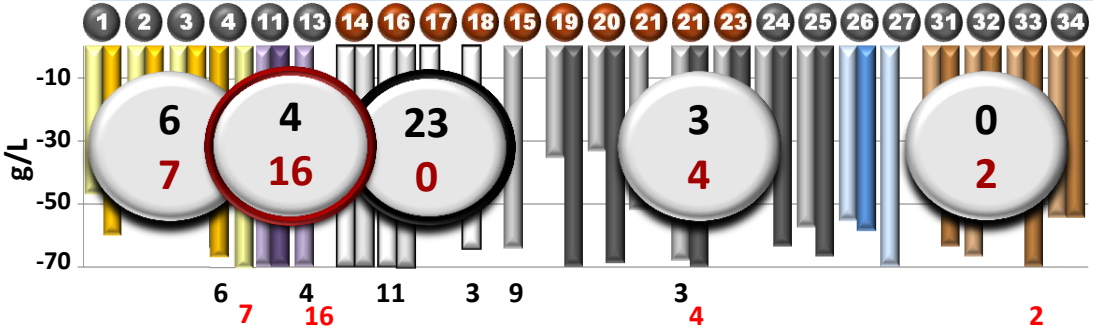


SAMPLES OF HYBRID VARIETIES FROM NON-ABANDONED VINEYARDS



SAMPLES OF HYBRID VARIETIES FROM ABANDONED VINEYARDS



CONCLUSIONS

Within this study we showed that the vineyards of the Azores islands harbor a **high yeast biodiversity** and a **high genetic diversity of *S. cerevisiae*** strains.

The comparison of the microflora from the different ecosystems of the islands showed **correlations between the predominating species, geographic location of the islands, type of vineyard and grape variety**.

The species ***H. uvarum* was predominant** in seven islands of the Azorean Archipelago, independent of the grape varieties and the type of vineyard. However, this species was present in **abandoned vineyards in considerably higher (20% more) proportions** than in non-abandoned vineyards.

CONCLUSIONS

The high percentage of ***C. zemplinina*** **in Santa Maria and São Miguel** differentiates the yeast microflora of this group of islands, pointing towards a **correlation between geographic origin of the grapes and the yeast microflora composition**.

The species ***M. pulcherrima,*** appears clearly associated with the **traditional grape varieties**, being only found in Graciosa and Pico, the islands with higher proportion of such grape varieties.

However, these data will be completed with results obtained from the samples collected in 2010.

CONCLUSIONS

The genetic diversity of *S. cerevisiae* was **more dependent on the sampling year** than on the geographic origin, grape variety or type of vineyard, showing that ecologically meaningful affirmations require repeated sampling campaigns.

This points to additional **biotic and abiotic factors** that affect the distribution and abundance of yeast communities in vineyards of the Azorean islands.

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